Utilization of microsatellite markers in rubber tree for genetic diversity analysis and genetic mapping of agronomic traits

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ABSTRACT

A total of 418 microsatellite markers have been developed in rubber tree at Cirad, mostly from enriched libraries. They are predominantly dinucleotidic markers with AG/CT or AC/GT repeats, and from non coding genomic DNA. 365 of these markers are polymorphic. Two examples of their use are illustrated here. Firstly, in order to assess the structure of genetic diversity among wild Amazonian rubber tree populations, a sample of 307 genotypes from 21 locations was analyzed with 15 microsatellite markers, each one located on a different linkage group. Two types of statistical analysis gave a convergent representation of genetic diversity, with a structure fashioned by hydrographical network and isolation by distance. Secondly, a genetic linkage map was established by genotyping 298 progenies from a cross between a cultivar resistant to South American Leaf Blight and a susceptible cultivar. This linkage map encompasses 177 markers and reaches a total length of 2053 centiMorgan. The determination of the resistance status of each of the progenies through the assessment of various parameters under controlled and field infestation conditions allowed the identification of a major resistance gene located on linkage group 15, an important resistance QTL on linkage group 13 and four minor resistance QTLs. These results will be exploited in a near future in a MAS breeding program aiming at developing new cultivars with high latex productivity combined with durable SALB resistance. Continuation of these works requires less variable markers, such as microsatellite located in expressed genes and SNPs. Numerous markers of these two types could easily be detected through sequencing of rubber tree, either whole genome, EST or BAC sequencing.